

## SEQUENCE LISTING

(1)

### GENERAL INFORMATION

(i) APPLICANT: NOBUTO YAMAMOTO

(ii) TITLE OF INVENTION: PREPARATION OF POTENT  
MACROPHAGE ACTIVATING FACTORS  
DERIVED FROM CLONED VITAMIN D  
BINDING PROTEIN AND ITS DOMAIN  
AND THEIR THERAPEUTIC USAGE  
FOR CANCER, HIV-INFECTION AND  
OSTEOPETROSIS

(iii) NUMBER OF SEQUENCES: 3

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: CAESAR, RIVISE, BERNSTEIN,  
COHEN & POKOTILOW, LTD.  
(B) STREET: 1635 Market Street, 12th Floor  
(C) CITY: Philadelphia  
(D) STATE: PA  
(E) COUNTRY: USA  
(F) ZIP: 19103-2212

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Diskette-3.5 inch, 1.44 Mb  
(B) COMPUTER: IBM PC Compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: WORDPERFECT VERSION 4.2

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:  
(B) FILING DATE: March 19, 1996  
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/478,121  
(B) FILING DATE: 07-JUNE-1995

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Robert S. Silver  
(B) REGISTRATION NO.: 35,681  
(C) REFERENCE/DOCKET NUMBER: Y1004/20002

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (215) 567-2010  
(B) TELEFAX: (215) 751-1142

(2) INFORMATION FOR SEQ ID NO: 1:

[i] SEQUENCE CHARACTERISTICS:

[A] LENGTH: 458 amino acids  
[B] TYPE: amino acid  
[D] TOPOLOGY: linear

[ii] MOLECULE TYPE: protein  
 [ii] HYPOTHETICAL: no  
 [vi] ORIGINAL SOURCES:  
 [A] ORGANISM: Human  
 [B] INDIVIDUAL/ISOLATE: Vitamin D-binding protein  
 (Gc protein)  
 [x] PUBLICATION INFORMATION:  
 [A] AUTHORS: Cooke, Nancy E., David, E Vivek  
 [B] TITLE: Serum Vitamin D-binding Protein is a  
 Third Member of the Albumin and Alpha  
 Fetoprotein Gene Family  
 [C] JOURNAL: J. Clinical Investigation  
 [D] VOLUME: 76  
 [E] ISSUE: 12  
 [F] PAGES: 2420-2424  
 [G] DATE: December, 1985  
 [K] RELEVANT RESIDUES IN SEQ ID NO:1: FROM 1-485

Leu	Glu	Arg	Gly	Arg	Asp	Tyr	Glu	Lys	Asn	Lys	Val	Cys	Lys	Glu	Phe	5	10	15
Ser	His	Leu	Gly	Lys	Glu	Asp	Phe	Thr	Ser	Leu	Ser	Leu	Val	Leu	Tyr	20	25	30
Ser	Arg	Lys	Phe	Pro	Ser	Gly	Thr	Phe	Glu	Gln	Val	Ser	Gln	Leu	Val	35	40	45
Lys	Glu	Val	Val	Ser	Leu	Thr	Glu	Ala	Cys	Cys	Ala	Glu	Gly	Ala	Asp	50	55	60
Pro	Asp	Cys	Tyr	Asp	Thr	Arg	Thr	Ser	Ala	Leu	Ser	Ala	Lys	Ser	Cys	65	70	75
Glu	Ser	Asn	Ser	Pro	Phe	Pro	Val	His	Pro	Gly	Thr	Ala	Glu	Cys	Cys	85	90	95
Thr	Lys	Glu	Gly	Leu	Glu	Arg	Lys	Leu	Cys	Met	Ala	Ala	Leu	Lys	His	100	105	110
Gln	Pro	Gln	Glu	Phe	Pro	Thr	Tyr	Val	Glu	Pro	Thr	Asn	Asp	Glu	Ile	115	120	125
Cys	Glu	Ala	Phe	Arg	Lys	Asp	Pro	Lys	Glu	Tyr	Ala	Asn	Gln	Phe	Met	130	135	140
Trp	Glu	Tyr	Ser	Thr	Asn	Tyr	Glu	Gln	Ala	Pro	Leu	Ser	Leu	Leu	Val	145	150	155
Ser	Tyr	Thr	Lys	Ser	Tyr	Leu	Ser	Met	Val	Gly	Ser	Cys	Cys	Thr	Ser	165	170	175
Ala	Ser	Pro	Thr	Val	Cys	Phe	Leu	Lys	Glu	Arg	Leu	Gln	Leu	Lys	His	180	185	190

Leu	Ser	Leu	Leu	Thr	Thr	Leu	Ser	Asn	Arg	Val	Cys	Ser	Gln	Tyr	Ala	
		195					200					205				
Ala	Tyr	Gly	Glu	Lys	Lys	Ser	Arg	Leu	Ser	Asn	Leu	Ile	Lys	Leu	Ala	
	210					215					220					
Gln	Lys	Val	Pro	Thr	Ala	Asp	Leu	Glu	Asp	Val	Leu	Pro	Leu	Ala	Glu	
225					230					235					240	
Asp	Ile	Thr	Asn	Ile	Leu	Ser	Lys	Cys	Cys	Glu	Ser	Ala	Ser	Glu	Asp	
				245					250					255		
Cys	Met	Ala	Lys	Glu	Leu	Pro	Glu	His	Thr	Val	Lys	Leu	Cys	Asp	Asn	
			260					265					270			
Leu	Ser	Thr	Lys	Asn	Ser	Lys	Phe	Glu	Asp	Cys	Cys	Gln	Glu	Lys	Thr	
		275					280					285				
Ala	Met	Asp	Val	Phe	Val	Cys	Thr	Tyr	Phe	Met	Pro	Ala	Ala	Gln	Leu	
	290					295					300					
Pro	Glu	Leu	Pro	Asp	Val	Arg	Leu	Pro	Thr	Asn	Lys	Asp	Val	Cys	Asp	
305					310					315					320	
Pro	Gly	Asn	Thr	Lys	Val	Met	Asp	Lys	Tyr	Thr	Phe	Glu	Leu	Ser	Arg	
				325					330					335		
Arg	Thr	His	Leu	Pro	Glu	Val	Phe	Leu	Ser	Lys	Val	Leu	Glu	Pro	Thr	
			340					345					350			
Leu	Lys	Ser	Leu	Gly	Glu	Cys	Cys	Asp	Val	Glu	Asp	Ser	Thr	Thr	Cys	
		355				360						365				
Phe	Asn	Ala	Lys	Gly	Pro	Leu	Leu	Lys	Lys	Glu	Leu	Ser	Ser	Phe	Ile	
	370					375					380					
Asp	Lys	Gly	Gln	Glu	Leu	Cys	Ala	Asp	Tyr	Ser	Glu	Asn	Thr	Phe	Thr	
385					390					395					400	
Glu	Tyr	Lys	Lys	Lys	Leu	Ala	Glu	Arg	Leu	Lys	Ala	Lys	Leu	Pro	Glu	
				405					410					415		
Ala	Thr	Pro	Thr	Glu	Leu	Ala	Lys	Leu	Val	Asn	Lys	Arg	Ser	Asp	Phe	
			420					425					430			
Ala	Ser	Asn	Cys	Cys	Ser	Ile	Asn	Ser	Pro	Pro	Leu	Tyr	Cys	Asp	Ser	
		435					440					445				
Glu	Ile	Asp	Ala	Glu	Leu	Lys	Asn	Ile	Leu							
	450					455			458							

[2] INFORMATION FOR SEQ ID NO: 2:

[i] SEQUENCE CHARACTERISTICS:

- [A] LENGTH: 89 amino acids
- [B] TYPE: amino acid
- [D] TOPOLOGY: linear

[ii] MOLECULE TYPE: protein

[ii] HYPOTHETICAL: no

[vi] ORIGINAL SOURCES:

- [A] ORGANISM: Human
- [B] INDIVIDUAL/ISOLATE: Vitamin D-binding protein (Gc protein)

[x] PUBLICATION INFORMATION:

- [A] AUTHORS: Cooke, Nancy E., David, E Vivek
- [B] TITLE: Serum Vitamin D-binding Protein is a Third Member of the Albumin and Alpha Fetoprotein Gene Family
- [C] JOURNAL: J. Clinical Investigation
- [D] VOLUME: 76
- [E] ISSUE: 12
- [F] PAGES: 2420-2424
- [G] DATE: December, 1985
- [K] RELEVANT RESIDUES IN SEQ ID NO:2: FROM 1 TO 4 and 5 TO 89

Leu	Glu	Arg	Gly	Pro	Leu	Leu	Lys	Lys	Glu	Leu	Ser	Ser	Phe	Ile	Asp	5	10	15
Lys	Gly	Gln	Glu	Leu	Cys	Ala	Asp	Tyr	Ser	Glu	Asn	Thr	Phe	Thr	Glu	20	25	30
Tyr	Lys	Lys	Lys	Leu	Ala	Glu	Arg	Leu	Lys	Ala	Lys	Leu	Pro	Glu	Ala	35	40	45
Thr	Pro	Thr	Glu	Leu	Ala	Lys	Leu	Val	Asn	Lys	Arg	Ser	Asp	Phe	Ala	50	55	60
Ser	Asn	Cys	Cys	Ser	Ile	Asn	Ser	Pro	Pro	Leu	Tyr	Cys	Asp	Ser	Glu	65	70	75
Ile	Asp	Ala	Glu	Leu	Lys	Asn	Ile	Leu								85	89	

[3] INFORMATION FOR SEQ ID NO: 3:

[i] SEQUENCE CHARACTERISTICS:

  [A] LENGTH: 88 amino acids

  [B] TYPE: amino acid

  [D] TOPOLOGY: linear

[ii] MOLECULE TYPE: protein

[ii] HYPOTHETICAL: no

[vi] ORIGINAL SOURCES:

  [A] ORGANISM: Human

  [B] INDIVIDUAL/ISOLATE: Vitamin D-binding protein (Gc protein)

[x] PUBLICATION INFORMATION:

  [A] AUTHORS: Cooke, Nancy E., David, E Vivek

  [B] TITLE: Serum Vitamin D-binding Protein is a Third Member of the Albumin and Alpha Fetoprotein Gene Family

  [C] JOURNAL: J. Clinical Investigation

  [D] VOLUME: 76

  [E] ISSUE: 12

  [F] PAGES: 2420-2424

  [G] DATE: December, 1985

  [K] RELEVANT RESIDUES IN SEQ ID NO:3: FROM 10 TO 94

Ile	Ile	Pro	Val	Glu	Glu	Glu	Asn	Pro	Pro	Leu	Leu	Lys	Lys	Glu	Leu	5	10	15
Ser	Ser	Phe	Ile	Asp	Lys	Gly	Gln	Glu	Leu	Cys	Ala	Asp	Tyr	Ser	Glu	20	25	30
Asn	Thr	Phe	Thr	Glu	Tyr	Lys	Lys	Lys	Leu	Ala	Glu	Arg	Leu	Lys	Ala	35	40	45
Lys	Leu	Pro	Glu	Ala	Thr	Pro	Thr	Glu	Leu	Ala	Lys	Leu	Val	Asn	Lys	50	55	60
Arg	Ser	Asp	Phe	Ala	Ser	Asn	Cys	Cys	Ser	Ile	Asn	Ser	Pro	Pro	Leu	65	70	75
Tyr	Cys	Asp	Ser	Glu	Ile	Asp	Ala	Glu	Leu	Lys	Asn	Ile	Leu			85	90	94